SEQUENCE LISTING

(1) GENERAL INFORMATION:

| | | \$) A | (A) (B) (C) (E) (F) | STRE CITY COUN POST. TELE | : sa ET: : PA TRY: AL CO PHONI | 32-3 RIS FRA ODE E: 0 | 4 ru NCE (ZIP 1 53 |): 7 77 | 5008 40 0 | • | | • | | | | | |
|------------------|------------------|------------------|----------------------------------|---------------------------------------|---|-----------------------------------|-----------------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------|------------------|-------|-----|
| | (i | i) T | ITLE | OF | INVE | OITE | N: S | R-p7 | 0 | | | | | | | | |
| | (ii. | i) N | UMBE: | R OF | SEQ | JENC | ES: | 40 | | | | | | | | | |
| | (i | | (A) 1 (B) ((C) (| MEDI COMPT OPERA | READI M TY UTER: ATINO VARE: | PE: BBI Sys | Flor M PC STEM | comp | patil DOS | MS-I | oos 1.0, | Vers | sion | #1.2 | 25 (E | EPO) | |
| (2) | INE | FORM | ATIOI | V FOR | R SEC | 3 7/2 | NO: | 1: | | | | | | | | | |
| | | | (A) I (B) I (C) S (D) I | LENGT TYPE: STRAN TOPOL | HARA H: 2 nuc IDEDN LOGY: | 874 leid ESS: lir | date | pai d | irs | | | | | | | | |
| | (ii | .) MC | DLECU | JLE I | YPE: | c ^{DNA} | | | | | | | | | | | |
| | (vi | | | | OURC | | ou s a | peljl | .a\ | | | | | ٠. | | | |
| | | (| B) L | AME / | KEY: ION: ESCR | 156 | 20 | | ID N | 0: 1 | <i>)</i> | ٠ | | | | | |
| TGC | CTCC | CCG | CCCG | CGCA | CC C | GCCC | CGAG | G CC | TGTG | CTCC | TGC | GAAG | ccc | ACGC | acc. | . A A | 60 |
| | GGGG | | | | | | | | | | | | | | | | 120 |
| | GCGA | | | | | | | | | | | \ | | | | GC | 173 |
| | | | | | | | | | 1 | Met . 1 | Ala | e1y/ | Ser \ | Thr 5 | Thr | | 17. |
| ACC Thr | TCC Ser | CCC | GAT Asp 10 | GGG Gly | GGC Gly | ACC Thr | ACG Thr | TTT Phe 15 | GAG Glu | CAC His | CTC Leu | TGG Trp | AGC Ser 20 | TCT Ser | CTG Leu | | 221 |
| GAA Glu | CCA Pro | GAC Asp 25 | AGC Ser | ACC Thr | TAC Tyr | TTC Phe | GAC Asp 30 | CTT Leu | CCC Pro | CAG Gln | TCA Ser | AGC Ser 35 | CGG Arg | ea à | AAT Asn | | 269 |
| AAT Asn | GAG Glu 40 | GTG Val | GTG Val | GGT Gly | GGC Gly | ACG Thr 45 | GAT Asp | TCC Ser | AGC Ser | ATG Met | GAC Asp 50 | GTC Val | TTC Phe | CAC His | CTA Leu | | 317 |
| GAG Glu 55 | GGC Gly | ATG Met | ACC Thr | ACA Thr | TCT Ser 60 | GTC Val | ATG Met | GCC Ala | CAG Gln | TTC Phe 65 | AAT Asn | TTG Leu | CTG Leu | AGC Ser | AGC Ser 70 | | 365 |
| ACC Thr | ATG Met | GAC Asp | CAG Gln | ATG Met 75 | AGC Ser | AGC Ser | CGC Arg | GCT Ala | GCC Ala .80 | TCG Ser | GCC Ala | AGC Ser | CCG Pro | TAC Tyr | ACC Thr | ` | 413 |

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| | CCC Pro | GAC Glu | G CAG | 5 Al | a Alá | AGC A Sei | C GTG r Val | CCC Pro | ACC Thi | His | TCA Ser | CCC Pro | TAC Ty: | GC: R Al. | a Gli | G CCC n Pro | | 461 | |
|---|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------|-------------------|-------------------|-------------------|---|-----------------|---|
| | AGC Ser | se) | Th: | r Phe | C GAC B Asp | ACC Thi | ATG Met | Ser 110 | Pro | GCC Ala | CCI Pro | GTC Val | 116 115 | Pro | C TCC Sei | I AAC r Asn | | 509 | |
| | ACC Thr | GA0 Asp 120 | Ty | Pro | GGA Gly | A CCC | CAC His 125 | His | TTC Phe | GAG Glu | GTC Val | ACT Thr 130 | Phe | CAC Glr | G CAC | TCC Ser | | 5 57 | |
| | 135 | Thr | Ala | a.Lys | Ser | 140 | Thr | Trp | Thr | Tyr | 145 | Pro | Leu | Leu | Lys | AAA Lys 150 | | 605 | |
| | CTC Leu | TAC | TGC Cys | GAC Glr | 111e | ∖ Ala | AAG Lys | ACA Thr | TGC Cys | CCC Pro 160 | Ile | CAG Gln | ATC Ile | Lys | GTC Val 165 | | | 653 | |
| | GCC Ala | CCA Pro | CCG Pro | Pro 170 | Pro | 61 y | ACC | GCC Ala | ATC Ile 175 | CGG Arg | GCC Ala | ATG Met | Pro | GTC Val 180 | Tyr | AAG Lys | | 701 | |
| | AAG Lys | GCG Ala | GAG Glu 185 | His | GTG Val | ACC Thr | GAC Asp | ATC Ile 190 | GTG Val | AAG Lys | CGC Arg | TGC - Cys | Pro 195 | Asn | CAC | GAG Glu | | 749 | |
| | CTC Leu | GGG Gly 200 | Arg | GAC Asp | TTC Phe | AAC | GAA Glu 205 | GGA Gly | CAG Gln | TCT Ser | GCC Ala | CCA Pro 210 | GCC Ala | AGC Ser | CAC His | CTC Leu | | 797 | |
| | ATC Ile 215 | CGT Arg | GTG Val | GAA Glu | GGC Gly | AAT Asn 220 | AAT Asn | CTC Leu | TCG Ser | CAG | TAT Tyr 225 | GTG Val | GAC Asp | GAC Asp | CCT Pro | GTC Val 230 | | 8 4 5 | |
| | ACC Thr | GGC Gly | AGG Arg | CAG Gln | AGC Ser 235 | GTC Val | GTG Val | GTG Val | CCC Pro | TAT Tyr 240 | GAG Glu | CCA Pro | CCA | CAG | GTG Val 245 | GGG Gly | | 993 | |
| | ACA Thr | GAA Glu | TTC Phe | ACC Thr 250 | ACC Thr | ATC Ile | CTG Leu | Tyr | AAC Asn 255 | TTC Phe | ATG Met | TGT CV3 | AAC Asn | AGC Ser 260 | AGC Ser | TGT | | 9,41 | |
| • | GTG Val | GGG Gly | GGC Gly 265 | ATG Met | AAC Asn | CGA Arg | CGG | CCC Pro 270 | ATC Ile | CTC Leu | ATC Ile | ATC | I Le 279 | ACC Thr | CTG Leu | GAG Glu | | 989 | |
| | ACG Thr | CGG Arg 280 | GAT Asp | GGG Gly | CAG Gln | GTG Val | CTG Leu 285 | GGC Gly | CGC Arg | CGG Arg | TCC Ser | TTC Phe 290 | GAG Glu | G1 % | CGC Arg | ATC Ile | | 1037 | |
| | TGC Cys 295 | GCC Ala | TGT Cys | CCT Pro | GGC Gly | CGC Arg 300 | GAC Asp | CGA Arg | AAA Lys | GCC Ala | GAT Asp 305 | GAG Glu | GAC Asp | CAC His | TAC Tyr | 370 yra cee | | 1085 | |
| | GAG Glu | CAG Gln | CAG Gln | GCC Ala | TTG Leu 315 | AAT Asn | GAG Glu | AGC Ser | TCC Ser | GCC Ala 320 | AAG Lys | AAC Asn | GGG Gly | GCT Ala | GCC Ala 325 | Ser | | 1133 | |
| | AAG Lys | CGC Arg | GCC Ala | TTC Phe 330 | AAG Lys | CAG Gln | AGT Ser | CCC Pro | Pro 335 | GCC Ala | GTC Val | CCC Pro | GCC Ala | CTG Leu 340 | GGC Gly | CCG Pro | ` | 181 | |
| , | σιγ | val | 345 | гуз | Arg | Arg | | Gly 350 | Asp | Glu | Asp | Thr | Tyr 355 | Tyr | Leu | Gln | | 1229 | ` |
| • | val. | CGA Arg 360 | GGC Gly | CGC Arg | GAG Glu | AAC Asn | TTC Phe 365 | GAG . Glu | ATC Ile | CTG Leu | ATG Met | AAG Lys 370 | CTG Leu | AAG Lys | GAG Glu | AGC Ser | | 1277 | |
| | | | | | | | | | | | | | | | | | | | |

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| | CTC Let 375 | 1 GI | G CTO | J ATO | G GAC | TTC Leu 380 | ı Val | CCC. Pro | G CAC | G CCC | CTC Leu 385 | ı Val | A GAC L Asp | TCO Ser | TA | CGG Arg 390 | 13.25 |
|---|-------------------|-------------------|-----------------------|--------------------|-----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------|
| | CAC Gl: | G CAC n Gli | CAC n Gli | G CAC | G CTC n Leu 395 | ı Leu | CAG Gln | AGG Arg | CCG Pro | AGT Ser 400 | His | CTA Leu | CAG Gln | CCC Pro | CCA Pro 405 | A TCC Ser | 1373 |
| | TAC Tyr | GG(| G CCC | 5 TC Val 418 | L Leu | TCG Ser | CCC Pro | ATG Met | AAC Asn 415 | Lys | GTG Val | CAC His | GGG Gly | GGC Gly 420 | Val | AAC Asn | 1421 |
| | AAC Lys | CTC Lev | 9 CCC 1 Pro 425 | Sez | Val | AAC Asn | CAG Gln | CTG Leu 430 | Val | Gly GGC | CAG Gln | CCT Pro | CCC Pro 435 | CCG Pro | CAC | AGC Ser | 1469 |
| | TCC | GCA Ala 440 | ı Ala | AÇA Thr | CCC Pro | AAC Asn | CTG Leu 445 | Gly | CCT Pro | GTG Val | GGC Gly | TCT Ser 450 | Gly | ATG Met | CTC | AAC Asn | 1517 |
| | AAC Asn 455 | His | GGC Gly | CAC His | GCA Ala | GTG Val 460 | PAO | GCC Ala | AAC Asn | AGC | GAG Glu 465 | ATG Met | ACC Thr | AGC Ser | AGC Ser | CAC His 470 | 1565 |
| | GGC Gly | ACC Thr | CAG Gln | TCC Ser | ATG Met 475 | Val | TCG Ser | ely gee | TCC Ser | CAC His 480 | TGC Cys | ACT Thr | CCG Pro | CCA Pro | CCC Pro 485 | CCC Pro | 1613 |
| | Tyr | His | Ala | 490 | Pro | Ser | Leu | Val | Sex 495 | Phe | Leu | Thr | Gly | Leu 500 | Gly | TGT Cys | 1661 |
| | Pro | Asn | Cy s 505 | Ile | Ģlu | TAT Tyr | Phe | Thr 510 | Ser | Gli | Gly | Leu | Gln 515 | Ser | Ile | Tyr | 1709 |
| | CAC His | CTG Leu 520 | CAG Gln | AAC Asn | CTG Leu | ACC Thr | ATC Ile 525 | GAG Glu | GAC Asp | CTG Leu | GI Å | GCC Ala 530 | CTG Leu | AAG Lys | ATC Ile | CCC | 1757 |
| / | GAG Glu 535 | CAG Gln | TAT Tyr | CGC Arg | ATG Met | ACC Thr 540 | ATC | TGG Trp | CGG Arg | GGC Gly | CTG Leu 545 | CAG Gln | GAC Asp | CTG Leu | AAG Lys | CAG Gln 550 | 1805 |
| | GGC Gly | CAC His | GAC Asp | TAC Tyr | GGC Gly 555 | GCC Ala | GCC Ala | GCG Ala | CAG Gln | CAG Gln 560 | CTG Leu | CTC Leu | CGG | TCC Ser | AGC Ser 565 | AAC Asn | 1853 |
| | | GCC Ala | | ATT Ile 570 | TCC Ser | ATC Ile | GGC Gly | GGC Gly | TCC Ser 575 | GGG Gly | GAG Glu | CTG Leu | CAG Gln | CGC Arg 580 | CAG | CGG Arg | 1901 |
| | GTC Val | ATG Met | GAG Glu 585 | GCC Ala | GTG Val | CAC His | TTC Phe | CGC Arg 590 | GTG Val | CGC Arg | CAC His | ACC Thr | ATC Ile 595 | ACC Thr | ATC Ile | CCC CCC | 1949 |
| | AAC Asn | CGC Arg 600 | GGC Gly | GGC Gly | CCC Pro | GGC Gly | GCC Ala 605 | GGC Gly | CCC Pro | GAC Asp | GAG Glu | TGG Trp 610 | GCG Ala | GAC Asp | TTC Phe | G1y | 1997 |
| | TTC Phe 615 | GAC Asp | CTG Leu | CCC Pro | GAC Asp | TGC Cys 620 | AAG Lys | GCC Ala | CGC Arg | Lys | CAG Gln 625 | CCC Pro | ATC . | AAG Lys | GAG Glu | GAG Glu 630 | 2045 |
| | TTC Phe | ACG Thr | GAG Glu | GCC Ala | GAG Glu 635 | ATC Ile | CAC His | TGAG | GGGC | CG G | GCCC. | AGCC | A GA | ĢCCT | GTGC | : | 2096 |
| | CACC | GCCC | AG A | .GACC | CAGG | c ca | CCTC | GCTC | TCC | TTCC | TGT (| GTCC. | AAAA | CT G | CCTC | CGGAG | 2156 |
| | GCAG | GGCC | TC C | AGGC | TGTG | c cc | GGGG | AAAG | GCA | AGGT | cce (| GCCC. | ATGC | cc c | GGCA | .CCTCA | 2216 |
| | | | | | | | | | | | | | | | | | |

| GAGAGGCCCA | GCCACCAAAG | CCGCCTGCGG | ACAGCCTGAG | TCACCTGCAG | 227 |
|------------|--|---|--|--|---|
| AGCTGCCCTA | ATGCTGGGCT | TGCGGGGCAG | GGGCCGGCCC | ACTCTCAGCC | 233 |
| CGGGCGTGCT | CCATGGCAGG | CGTGGGTGGG | GACCGCAGTG | TCAGCTCCGA | 239 |
| TCATCCTAGA | GACTCTGTCA | TCTGCCGATC | AAGCAAGGTC | CTTCCAGAGG | 245 |
| CTTCGCTGGT | GGACTGCCAA | AAAGTATTTT | GCGACATCTT | TTGGTTCTGG | 251 |
| GCAGCCAAGC | GACTGTGTCT | GAAACACCGT | GCATTTTCAG | GGAATGTCCC | 2576 |
| GGGACTCTCT | CTGCTGGACT | TGGGAGTGGC | CTTTGCCCCC | AGCACACTGT | 2636 |
| ACCGCCTCCT | TCCTGCCCCT | AACAACCACC | AAAGTGTTGC | TGAAATTGGA | 2696 |
| GAAGGCGCAA | CCCCTCCCAG | GTGCGGGAAG | CATCTGGTAC | CGCCTCGGCC | 2756 |
| AGCCTGGCCA | CAGTCACCTC | TCCTTGGGGA | ACCCTGGGCA | GAAAGGGACA | 2916 |
| AGAGGACCGG | AAATTGTCAA | TATTTGATAA | AATGATACCC | TTTTCTAC | 2874 |
| | AGCTGCCCTA CGGGCGTGCT TCATCCTAGA CTTCGCTGGT GCAGCCAAGC GGGACTCTCT ACCGCCTCCT GAAGGCGCAA AGCCTGGCCA | AGCTGCCCTA ATGCTGGGCT CGGGCGTGCT CCATGGCAGG TCATCCTAGA GACTCTGTCA CTTCGCTGGT GGACTGCCAA GCAGCCAAGC GACTGTGTCT GGGACTCTCT CTGCTGGACT ACCGCCTCCT TCCTGCCCCT GAAGGCGCAA CCCCTCCCAG AGCCTGGCCA CAGTCACCTC | AGCTGCCCTA ATGCTGGGCT TGCGGGGCAG CGGGCGTGCT CCATGGCAGG CGTGGGTGGG TCATCCTAGA GACTCTGTCA TCTGCCGATC CTTCGCTGGT GGACTGCCAA AAAGTATTTT GCAGCCAAGC GACTGTGTCT GAAACACCGT GGGACTCTCT CTGCTGGACT TGGGAGTGGC ACCGCCTCCT TCCTGCCCCT AACAACCACC GAAGGCGCAA CCCCTCCCAG GTGCGGGAAG AGCCTGGCCA CAGTCACCTC TCCTTGGGGA | AGCTGCCCTA ATGCTGGGCT TGCGGGGCAG GGGCCGGCCC CGGGCGTGCT CCATGGCAGG CGTGGGTGGG GACCGCAGTG TCATCCTAGA GACTCTGTCA TCTGCCGATC AAGCAAGGTC CTTCGCTGGT GGACTGCCAA AAAGTATTTT GCGACATCTT GCAGCCAAGC GACTGTGTCT GAAACACCGT GCATTTTCAG GGGACTCTCT CTGCTGGACT TGGGAGTGGC CTTTGCCCCC ACCGCCTCCT TCCTGCCCCT AACAACCACC AAAGTGTTGC GAAAGGCGCAA CCCCTCCCAG GTGCGGGAAG CATCTGGTAC AGCCTGGCCA CAGTCACCTC TCCTTGGGGA ACCCTGGGCA | AGGAGGCCCA GCCACCAAG CCGCCTGCGG ACAGCCTGAG TCACCTGCAG AGCTGCCCTA ATGCTGGGCT TGCGGGGCAG GGGCCGGCCC ACTCTCAGCC CGGGCGTGCT CCATGGCAGG CGTGGGTGGG GACCGCAGTG TCAGCTCCGA TCATCCTAGA GACTCTGTCA TCTGCCGATC AAGCAAGGTC CTTCCAGAGG CTTCGCTGGT GGACTGCCAA AAAGTATTTT GCGACATCTT TTGGTTCTGG GCAGCCAAGC GACTGTGTCT GAAACACCGT GCATTTTCAG GGAATGTCCC GGGACTCTCT CTGCTGGACT TGGGAGTGGC CTTTGCCCCC AGCACACTGT ACCGCCTCCT TCCTGCCCCT AACAACCACC AAAGTGTTGC TGAAATTGGA GAAGGCCAAA CCCCTCCCAG GTGCGGGAAG CATCTGGTAC CGCCTCGGCC AGCCTGGCCA CAGTCACCTC TCCTTGGGGA ACCCTGGGCA GAAAGGGACA AGAGGACCGG AAATTGTCAA TATTTGATAA AATGATACCC TTTTCTAC |

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 amino acids
 - (B) TYPE: amind acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gln Ser Thr Thr Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
50 55

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala 100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr 130 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro 145 150 155

Ile Gln Ile Lys Val Ser Ala Pro Pro Pro Pro Gly Thr Ala Ile Arg 165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys
180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln S r

(mb

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asq Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg 275 280 285 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala 290 295 300 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala 305 310 320 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala 325 Val Pro Ala Leu Gly Pro Gly Val Lys Lys Arg Arg His Gly Asp Glu 340 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu 355 Met Lys Leu Lys Glu Ser Leu Glu Leu Wet Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser 385 400 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420 425 430 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His Gly Thr Gln Ser Met Val Ser Gly Ser His 465 Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe 485 490 495 Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln 500 505 510 Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Gly Ala Ala Ala Gln Gln 545 550 555 560 Leu Leu Arg Ser Ser Asn Ala Ala Ala Ile Ser Ile Gly Gly Ser Gly 565 570 575 Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg

585

His Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Ala Gly Pro Asp

580

ACC GAC TAT CCC GGA CCC CAC CAC TTC GAG GTC ACT TTC CAG CAG TCC

Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser

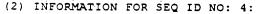
AGC ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCA CTC TTG AAG AAA

557

605

| Se 13 | r Th 5 | r Al | a Ly | s Se | r Ala 140 | a Thr | Trp | Thi | r Tyr | Ser 145 | Pro | Le | ı Let | L Ly | s Lys 150 | | |
|-------------------|---------------------|--------------------|-----------------------|-----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|------|
| CT Le | C TA | c TG | C CAG s Gli | 3 ATC n Ile 159 | e Ala | AAC A Lys | ACA Thr | L TGC | CCC Pro 160 | Ile | CAG Gln | ATC | Lys | GT0 Va: 16: | G TCC l Ser | | 653 |
| GC all | a. 5 t. | A CC | G CC0 0 Pro 170 | o Pro | G GG(| ACC Thr | GCC Ala | 175 | Arg | GCC Ala | ATG Met | CC1 | GTC Val | Ty | AAG Lys | | 701 |
| AA(Ly: | G GCd S Ala | GA(2 G1) 18 | a His | GTC Val | G ACC | GAC Asp | Ile 190 | Val | AAG Lys | CGC | TGC Cys | CCC Pro | Asn | CAC His | GAG Glu | | 749 |
| CTO | GG(1 Gly 200 | Arq | SAC YEA | Phe | AAC Asr | GAA Glu 205 | Gly | CAG Gln | TCT Ser | GCC Ala | CCA Pro 210 | Ala | AGC | CAC | CTC Leu | | 797 |
| ATC 116 215 | Arc | GTO Val | G GAA | . GSC | AAT Asn 220 | Asn | CTC Leu | TCG Ser | CAG Gln | TAT Tyr 225 | GTG Val | GAC Asp | GAC Asp | CCI | GTC Val 230 | | 845 |
| ACC Thr | GGC Gly | AGO Aro | G CAG | AGC Ser 235 | · Val | GTG Val | GTG Val | CCC | TAT Tyr 240 | GAG Glu | CCA Pro | CCA Pro | CAG Gln | GTG Val 245 | GGG Gly | | 893 |
| ACA Thr | GAA Glu | TTC Phe | ACC Thr 250 | Thr | ATC | CTG Leu | TAC Tyr | AAC Asn 255 | TTC Phe | ATG Met | TGT Cys | AAC Asn | AGC Ser 260 | AGC | TGT | | 941 |
| GTG Val | GGG Gly | GGC Gly 265 | Met | AAC Asn | CGA Arg | CGG Arg | CCC Pro 270 | ATC 11e | CTC Leu | ATC Ile | ATC Ile | ATC Ile 275 | ACC Thr | CTG Leu | GAG Glu | | 989 |
| ACG Thr | CGG Arg 280 | Asp | GGG Gly | CAG Gln | GTG Val | CTG Leu 285 | GGC Gly | CGC Arg | Arg coe | TCC | TTC Phe 290 | GAG Glu | GGC | CGC | ATC Ile | | 1037 |
| TGC Cys 295 | GCC Ala | TGT Cys | CCT Pro | GGC | CGC Arg 300 | GAC Asp | CGA Arg | AAA Lys | GCC Ala | GAT Asp 305 | GAG Glu | GAC Asp | CAC His | TAC Tyr | CGG Arg 310 | | 1085 |
| GÁG Glu | CAG Gln | CAG Gln | GCC Ala | TTG Leu 315 | AAT Asn | GAG Glu | AGC Ser | TCC Ser | GCC Ala 320 | AAG Lys | AAC Asn | ez ece | GCT Ala | GCC Ala 325 | AGC Ser | | 1133 |
| AAG Lys | CGC Arg | GCC Ala | TTC Phe 330 | Lys | CAG Gln | AGT Ser | CCC Pro | CCT Pro 335 | GCC Ala | GTC Val | CCC Pro | GCC Ala | CTG Leu 340 | GGC Gly | CCG Pro | | 1191 |
| GGT Gly | GTG Val | AAG Lys 345 | AAG Lys | CGG Arg | CGG Arg | CAC His | GGA Gly 350 | GAC Asp | GAG Glu | GAC Asp | ACG Thr | TAC Tyr 355 | TAC Tyr | C TG Leu | CAG Gln | | 1229 |
| GTG Val | CGA Arg 360 | GGC Gly | CGC Arg | GAG Glu | AAC Asn | TTC Phe 365 | GAG Glu | ATC Ile | CTG Leu | ATG Met | AAG Lys 370 | CTG Leu | AAG Lys | GAG Glu | AOC Ser | \ | 1277 |
| CTG Leu 375 | GAG Glu | CTG Leu | ATG Met | GAG Glu | TTG Leu 380 | GTG Val | CCG Pro | CAG Gln | CCG Pro | CTG Leu 385 | GTA Val | GAC Asp | TCC Ser | TAT Tyr | CGG Arg 390 | | 1325 |
| CAG Gln | CAG Gln | CAG Gln | CAG Gln | CTC Leu 395 | CTA Leu | CAG . Gln . | AGG Arg | CCG Pro | AGT Ser 400 | CAC His | CTA Leu | CAG Gln | CCC Pro | CCA Pro 405 | TCC Ser | | 373 |
| TAC Tyr | GGG Gly | CCG Pro | GTC Val 410 | CTC Leu | TCG Ser | CCC . Pro | Met . | AAC Asn 415 | AAG Lys | GTG Val | CAC (| GGG Gly | GGC Gly 420 | GTG Val | AAC Asn | | 1421 |
| AAG | CTG | CCC | TCC | GTC | AAC | CAG | CTG | GTG | GGC (| CAG | CCT (| ccc | CCG | CAC | AGC | | 1469 |

| Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser | |
|---|--------|
| TCG GCA GCT ACA CCC AAC CTG GGA CCT GTG GGC TCT GGG ATG CTC AAC Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn 440 450 | 1517 |
| AAC CAC GGC CAC GCA GTG CCA GCC AAC AGC GAG ATG ACC AGC AGC CAC ASN His Gly His Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His 455 | 1565 |
| GGC ACC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA CCC Gly Thr Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro 435 485 | 1613 |
| TAC CAC GCC GAC CCC AGC CTC GTC AGG ACC TGG GGG CCC TGAAGATCCC Tyr His Ala Asp Pro Ser Leu Val Arg Thr Trp Gly Pro 490 495 | 1662 |
| CGAGCAGTAT CGCATGACCA TCTGGCGGGG CCTGCAGGAC CTGAAGCAGG GCCACGACT | Á 1722 |
| CGGCGCCGCC GCGCAGCAGC TGCTGCGCTC CAGCAACGCG GCCGCCATTT CCATCGGCG | G 1782 |
| CTCCGGGGAG CTGCAGCGCC AGCGGGTCAT GGAGGCCGTG CACTTCCGCG TGCGCCACA | C 1842 |
| CATCACCATO COCAACOGOG GOGGCCCOO CGCCGGCCCC GACGAGTGGG CGGACTTCG | G 1902 |
| CTTCGACCTG CCCGACTGCA AGGCCCGCAA CCAGCCCATC AAGGAGGAGT TCACGGAGG | C 1962 |
| CGAGATCCAC TGAGGGGCCG GGCCCAGCCA GAGCCTGTGC CACCGCCCAG AGACCCAGG | C 2022 |
| CGCCTCGCTC TC | 2034 |



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Gln Ser Thr Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser 35

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala oln 50 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr 130 135 140



Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser Ala Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys
180 185 190 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser 195 200 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Pro Tyr 225 230 235 Glu Pro Pro Gln val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu 260 270 Ile Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg 275 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala 290 295 300 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala 305 310 315 320 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Pro Gly Val Lys Lys Arg Arg His Gly Asp Glu 340 345 350 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Gla Asn Phe Glu Ile Leu 355 360 365 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro 370 375 Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His Gly Thr Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr

(2) INFORMATION FOR SEQ ID NO: 5:

Trp Gly Pro

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2156 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(A) ORGANISM: Homo sapiens

(11) MOLECULE TYPE: cDNA
(V1) ORIGINAL SOURCE:

FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 33..1940 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: GCGAGCTGCC CTCGGAGGCC GGCGTGGGGA AG ATG GCC CAG TCC ACC GCC ACC 53 Met Ala Gln Ser Thr Ala Thr TCC CCT GAT GGG GGC ACC ACG TTT GAG CAC CTC TGG AGC TCT CTG GAA Ser Pro Asp Gly Gly Thr Thr Phe Glu His Leu Trp Ser Ser Leu Glu 101 15 CCA GAC AGC ACC TAC TTC GAC CTT CCC CAG TCA AGC CGG GGG AAT AAT 149 Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Ser Ser Arg Gly Asn Asn GAG GTG GTG GGC GGA ACG GAT TCC AGC ATG GAC GTC TTC CAC CTG GAG Glu Val Val Gly Gly Thr Asp ger Ser Met Asp Val Phe His Leu Glu 197 GGC ATG ACT ACA TCT GTC ATG GCC CAG TTC AAT CTG CTG AGC AGC GC Gly Met Thr Thr Ser Val Met Ala on Phe Asn Leu Leu Ser Ser Thr 245 ATG GAC CAG ATG AGC AGC CGC GCG GCC TCG GCC AGC CCC TAC ACC CCA Met Asp Gln Met Ser Ser Arg Ala Ala Ser Ala Ser Pro Tyr Thr Pro 293 80 GAG CAC GCC GCC AGC GTG CCC ACC CAC TCG CCC TAC GCA CAA CCC AGC 341 Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro Ser TCC ACC TTC GAC ACC ATG TCG CCG GCG CCT GTC ATC CCC TCC AAC ACC 389 Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr 110 GAC TAC CCC GGA CCC CAC CAC TTT GAG GTC ACT TTC CAG CAG TCC AGC 437 Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser Ser ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCG CTC TTG AAG AAA CTC 485 Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Lys Lys Leu TAC TGC CAG ATC GCC AAG ACA TGC CCC ATC CAG ATC AAG GTG TCC ACC 533 Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser Th CCG CCA CCC CCA GGC ACT GCC ATC CGG GCC ATG CCT GTT TAC AAG AAA 581 Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys 175 GCG GAG CAC GTG ACC GAC GTG GTG AAA CGC TGC CCC AAC CAC GAG CTC Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu GGG AGG GAC TTC AAC GAA GGA CAG TCT GCT CCA GCC AGC CAC CTC ATC Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His L u Ile 677 205

| | CG(Ar | C GT g Va | G GA 1 G1 | A GG u Gl | C AA' y Ası 220 | n Asr | CTC Let | I TCC | G CAC | G TA: | r Val | G GA | T GAG p Asj | p Pr | T GT 0 Va 23 | C ACC 1 Thr 0 | | 725 |
|---|-------------------|-----------------------|-------------------|----------------------|-----------------------|-------------------|-------------------|-----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------------|--------------------|---------------------|-----|-----|
| | GG(Gl) | C AGG Y Arg | G CA g Gl | G AG n Se . 23 | r Va. | C GTO l Val | GTC Val | G CCC | TA1 Ty1 240 | : Glu | CCA Pro | A CC | A CAG | G GT0 n Va: 249 | l Gl | G ACG y Thr | | 773 |
| | GAZ Glu | A TTO | C AC E Th | £ IU: | C ATO | C CTG E Leu | TAC Tyr | AAC Asn 255 | ı Ph∈ | ATC Met | TGT Cys | AAC Asi | 2 AGC | : Se | TG: | T GTA s Val | 8 | 821 |
| | GGC Gly | G GGG 7 Gly 265 | / Me | G AA(t Asi | Arg | G CGG J Arg | CCC Pro 270 | Ile | CTC Leu | ATC | ATC | 11e 275 | Thr | CTC Lev | G GAG | G ATG 1 Met | 8 | 69 |
| | CGG Arg 280 | , ASE | GGG Gly | G CAC y Glr | GTC Val | CTG Leu 285 | . Gly | CGC Arg | CGG Arg | TCC Ser | TTT Phe 290 | Glu | GGC Gly | CGC Arc | ATC | TGC Cys 295 | 9 | 17 |
| | GCC Ala | : TGT : Cys | Pro | r GGC o Gly | CGC Arg 300 | Asp | AIGA | AAA Lys | GCT Ala | GAT Asp 305 | Glu | GAC Asp | CAC His | TAC | CGC Arc 310 | GAG Glu | 9 | 65 |
| | CAG Gln | CAG Gln | GCC Ala | CTG Leu 315 | Asn | GAG Glu | AGC Ser | TCC Ser | GCC Ala 320 | Lys | AAC Asn | GGG Gly | GCC Ala | GCC Ala 325 | Ser | AAG Lys | 10 | 13 |
| | CGT Arg | GCC Ala | Phe | rys | CAG Gln | AGC Ser | CCC Pro | CCT Pro 335 | GCC Ala | GTC Val | CCC Pro | GCC Ala | CTT Leu 340 | Gly | GCC | GGT | 10 | 61 |
| | GTG Val | AAG Lys 345 | Lys | CGG Arg | CGG Arg | CAT His | GGA Gly 350 | GAC Asp | GAG Glu | GAQ Asp | ACG Thr | TAC Tyr 355 | TAC Tyr | CTT Leu | CAG | GTG Val | 11 | 09 |
| i | CGA Arg 360 | GGC Gly | CGG Arg | GAG Glu | AAC Asn | TTT Phe 365 | GAG Glu | ATC Ile | CTG Leu | ATG Met | AAG Lys 370 | CTG | AAA Lys | GAG Glu | AGC Ser | CTG Leu 375 | 11 | 57 |
| 1 | GAG Glu | CTG Leu | ATG Met | GAG Glu | TTG Leu 380 | GTG Val | CCG Pro | CAG Gln | CCA Pro | CTG Leu 385 | GTG Val | GAC Asp | TCC Ser | TAT | CGG Arg 390 | | 120 | |
| | CAG Gln | CAG Gln | CAG Gln | CTC Leu 395 | CTA Leu | CAG Gln | AGG Arg | CCG Pro | AGT Ser 400 | CAC His | CTA Leu | CAG Gln | CCC Pro | Pro 405 | TCC Ser | TAC | 125 | 5 3 |
| | GGG Gly | CCG Pro | GTC Val 410 | CTC Leu | TCG Ser | CCC Pro | ATG Met | AAC Asn 415 | AAG Lys | GTG Val | CAC His | GGG Gly | GGC Gly 420 | ATG Met | AAC neA | AAG Lys | 130 | 01 |
| | Leu | Pro 425 | TCC | GTC Val | AAC Asn | CAG Gln | CTG Leu 430 | GTG Val | GGC Gly | CAG Gln | CCT Pro | CCC Pro 435 | CCG Pro | CAC His | AGT Ser | TCG Ser | 134 | 19 |
| | GCA Ala 440 | GCT Ala | ACA Thr | CCC Pro | Asn | CTG Leu 445 | GGG Gly | CCC Pro | GTG Val | Gly | CCC Pro 450 | GGG Gly | ATG Met | CTC Leu | AAC Asn | AAC Asn 455 | 139 | 7 |
| | CAT His | GGC Gly | CAC His | GCA Ala | GTG Val 460 | CCA Pro | GCC . Ala . | AAC Asn | Gly | GAG Glu 465 | ATG Met | AGC Ser | AGC Ser | AGC Ser | CAC- His 470 | AGC Ser | 144 | 5 |
| | GCC Ala | CAG Gln | TCC Ser | ATG Met 475 | GTC Val | TCG (Ser (| GGG (Gly : | Ser : | CAC His 480 | TGC . Cys. | ACT Thr | CCG Pro | CCA Pro | CCC Pro 485 | CCC Pro | TAC Tyr | 149 | 3 |
| | CAC (| | GAC Asp 490 | CCC Pro | AGC Ser | CTC (Leu \ | val: | AGT (Ser 495 | TTT ' | ITA / | ACA (| Gly | TTG Leu 500 | GGG Gly | TGT Cys | CCA Pro | 154 | 1 |
| | | | | | | | | | | | | | | | | | | |

And OSA

| AAC Asn | TGC Cys 505 | ATC Ile | GAG Glu | TAT Tyr | TTC Phe | ACC Thr 510 | TCC Ser | CAA Gln | GGG Gly | TTA Leu | CAG Gln 515 | AGC Ser | ATT | TAC Tyr | CAC | | 1589 |
|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|------|
| CTG Leu 520 | 32G 318 | AAC Asn | CTG Leu | ACC Thr | ATT Ile 525 | GAG Glu | GAC Asp | CTG Leu | GGG Gly | GCC Ala 530 | CTG Leu | AAG Lys | ATC Ile | CCC Pro | GAG Glú 535 | | 1637 |
| CAG Gln | TAC | CG | ATG Met | ACC Thr 540 | ATC Ile | TGG Trp | CGG Arg | GGC GI'y | CTG Leu 545 | Gln | GAC | CTG Leu | AAG Lys | CAG Gln 550 | GGC Gly | | 1685 |
| CAC His | GAC Asp | TAC Tyr | AGC Ser 555 | ACC | GCG Ala | CAG Gln | CAG Gln | CTG Leu 560 | CTC Leu | CGC Arg | TCT Ser | AGC Ser | AAC Asn 565 | GCG Ala | GCC Ala | | 1733 |
| ACC Thr | ATC Ile | TCC Ser 570 | ATC Ile | GGC Gly | ejh gec | TCA Ser | GGG Gly 575 | GAA Glu | CTG Leu | CAG Gln | CGC Arg | CAG Gln 580 | CGG Arg | GTC Val | ATG Met | | 1791 |
| GAG Glu | GCC Ala 585 | GTG Val | CAC His | TTC Phe | CGC Arg | OTG Val 590 | CGC Arg | CAC His | ACC Thr | ATC Ile | ACC Thr 595 | ATC | CCC Pro | AAC Asn | CGC Arg | | 1829 |
| GGC G1 y 600 | GGC Gly | CCA Pro | GGC Gly | GGC Gly | GGC Gly 605 | CCT Pro | AAC AAP | GAG Glu | TGG Trp | GCG Ala 610 | GAC Asp | TTC Phe | GGC Gly | TTC Phe | GAC Asp 615 | | 1877 |
| CTG Leu | CCC Pro | GAC Asp | TGC Cys | AAG Lys 620 | GCC Ala | CGC Arg | AAG Lys | dAG GAn | CCC Pro 625 | ATC Ile | AAG Lys | GAG Glu | GAG Glu | TTC Phe 630 | ACG Thr | , | 1925 |
| GAG Glu | GCC Ala | GAG Glu | ATC Ile 635 | CAC His | TGAG | GGCC | TC G | CCTG | gC10 | C AG | CCTG | ccc | ACC | GCCC | AGA | | 1980 |
| GACC | CAAG | CT G | CCTC | CCCT | с тс | CTTC | CTGT | GTG | TCCA | AAA | CTGC | CTCA | .GG A | .GGCA | .GGAC | : | 2040 |
| TTCG | GGCT | GT G | cccG | GGGA | A AG | GCAA | GGTC | CGG | CCCA | icg/ | CCAG | GCAC | CT C | ACAG | GCCC | : | 2100 |
| AGGA | AAGG | CC C | AGCC. | ACCG. | A AG | CCGC | CTGT | GGA | CAGC | CTG | AGTC | ACCT | GC A | .GAAC | С | | 2156 |

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu 1 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 115 Val The Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Dys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser 195 200 205 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln 210 220 Tyr Val Asp Asp Pro Val Tha Gly Arg Gln Ser Val Val Pro Tyr 230 Glu Pro Pro Gln Val Gly Thr Gly Phe Thr Thr Ile Leu Tyr Asn Phe 250 Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu 260 270 Ile Ile Ile Thr Leu Glu Met Arg Asp Cly Gln Val Leu Gly Arg Arg 275 280 285 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala 290 295 300 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gla Ser Pro Pro Ala 325 330 335 Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg H\s Gly Asp Glu 340 345 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu 355 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro cin Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Thr Gly Leu Gly Cys Pro Aşn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Lev Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Deu Lys Ile Pro Glu Gin Tyr Arg Met Thr Ile Trp Arg Gly Gly Ala Leu Gln Asp' Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Sex Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His 580 Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His 630 (2) INFORMATION FOR SEQ ID NO: (i) SEQUENCE CHARACTERISTICS (A) LENGTH: 2040 base pairs

- (ii) MOLECULE TYPE: cDNA
- (Vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mus musculus
- (ix) FEATURE:

50

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1890

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGATCTCCCT GTGGCCTGCA GGGGACTGAG CCAGGGAGTA GATGCCCTGA GACCCCAAGG 60 GACACCCAAG GAAACCTTGC TGGCTTTGAG AAAGGGATCG TCTCTCTCT GCCCAAGAGA 120 AGC ATG TGT ATG GGC CCT GTG TAT GAA TCC TTG GGG CAG GCC CAG TTG 168 Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe AAT TTG CTC AGC AGT GCC ATG GAC CAG ATG GGC AGC CGT GCG GCC CCG 216 Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro GCG AGC CCC TAC ACC CCG GAG CAC GCC GCC AGC GCG CCC ACC CAC TCG 264 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser 40 CCC TAC GCG CAG CCC AGC TCC ACC TTC GAC ACC ATG TCT CCG GCG CCT Pro Tyr Ala Gln Pro Ser Ser Thr Ph Asp Thr M t Ser Pro Ala Pro 312

GTC ATC CCT TCC AAT ACC GAC TAC CCC GGC CCC CAC CAC TTC GAG GTC

| | | | | | | | | | | • | | | | | | | | | |
|--------|-------------------|-------------------|----------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------------------|---|-------------|
| | ۷a | 1 11 | .е 55 | Pro | Se | r As | n Th | r As ₁ | p Ty | r Pr | o G1 | y Pr | o Hi 7 | | s Ph | e Gl | u Val | | |
| | 3 | 2/50 | e ' | GIN | GII. | ı Se. | r Se. 8 | r Thi | r Al | a Ly | s Se | r Ala 90 | a Thi | r Tr | p Th | r Ty | C TCC r Ser 95 | | 408 |
| | | o Le | <u>"</u> | Leu | τÿs | 100 | s Let | ı Tyı | Cy: | s Gl | n Ile 105 | e Ala | Lys | 3 Thi | r Cy: | s Pr | C ATC O Ile | | 456 |
| | GA: | G AT n Il | e i | AAA Lys | GTC Val | . 2e1 | C ACA | A CCA | CCI Pro | A CCC Pro 120 | o Pro | GGC Gly | ACC Thr | GCC Ala | 125 | Ar | G GCC G Ala | | 504 |
| | AT(| G CC t Pr | 0 1 | GTC /al 130 | TAC | AAC | F AAC B Lys | G GCA B Ala | GA0 Glu 135 | ı His | GTG Val | ACC Thr | GAC Asp | ATT 11e | Val | Lys | G CGC B Arg | | 552 |
| | TG0 .Cys | CCG Pro 14 | O F | AAC Asn | CAC His | GAG Glu | CTI | GGA Gly 150 | AGG Arg | GAC Asp | TTC Phe | TAA neA | GAA Glu 155 | . Gly | CAC Glr | TC1 | GCC Ala | | 600 |
| | Pro 160 | AT | r A a.S | GC er | CAC His | CTC | Ile 165 | . A∕£a | GTA Val | GAA Glu | GGC Gly | AAC Asn 170 | Asn | CTC | GCC Ala | CAC Glr | TAC Tyr 175 | | 648 |
| | GTC Val | GA: | r G > A | AC .sp | CCT Pro | GTC Val 180 | Thr | GGA Gly | AGG | CAG Glm | AGT Ser 185 | GTG Val | GTT Val | GTG Val | CCG Pro | TAT Tyr 190 | GAA Glu | | 6 96 |
| | CCC Pro | CCA Pro | A C | Tu | GTG Val 195 | GĞA Gly | ACA Thr | GAA Glu | TTT Phe | The 200 | Thr | ATC Ile | CTG Leu | TAC Tyr | AAC Asn 205 | Phe | ATG Met | | 744 |
| | TGT Cys | AAC Asn | ıs | GC er 10 | AGC Ser | TGT | GTG Val | GGG Gly | GGC Gly 215 | ATG Met | YAA neA | CGG | AGG Arg | CCC Pro 220 | ATC Ile | CTT Leu | GTC Val | | 792 |
| | XTC Ile | ATC Ile 225 | . +1 | CC (| CTG Leu | GAG Glu | ACC Thr | CGG Arg 230 | TAD QeA | GGA Gly | CAG Gln | GTQ Val | CTG Leu 235 | GGC Gly | CGC Arg | CGG Arg | TCT Ser | | 840 |
| • | TTC Phe 240 | GAG Glu | G(| GT (| CGC Arg | ATC Ile | TGT Cys 245 | GCC Ala | TGT Cys | CCT Pro | GGC Gly | CGT Arg 250 | GAC Asp | ATA CCC | AAA Lys | GCT Ala | GAT Asp 255 | | 888 |
| (| GAA Glu | GAC Asp | C# | AT 7 | TAC Tyr | CGG Arg 260 | GAG Glu | CAA Gln | CAG Gln | GCT Ala | CTG Leu 265 | AAT Asn | GAA Glu | AGT Ser | ACC | ACC Thr 270 | AAA Lys | | 936 |
| F | TA/ ne/ | GGA Gly | GC Al | a r | GCC 11 a 275 | AGC Ser | AAA Lys | CGT Arg | GCA Ala | TTC Phe 280 | AAG Lys | CAG Gln | AGC Ser | CCC Pro | CCT Pro 285 | GCC Ala | ATC Ile | ٠ | 984 |
| Ē | Pro | GCC Ala | CT Le 29 | eu c | GT Gly | ACC Thr | AAC Asn | GTG Val | AAG Lys 295 | AAG Lys | AGA Arg | CGC | CAC His | GGG Gly 300 | GAC Asp | GAG Glu | GAC Asp | | 1032 |
| A | ITG et | TTC Phe 305 | TA Ty | C A | IET . | CAC His | GTG Val | CGA Arg 310 | GGC Gly | CGG Arg | GAG Glu | AAC Asn | TTT Phe 315 | GAG Glu | ATC Ile | TTG Leu | ATG Met | \ | 1080 |
| _ | AA .ys 20 | GTC Val | AA Ly | G G | AG . | AGC Ser | CTA Leu 325 | GAA Glu | CTG Leu | ATG Met | GAG Glu | CTT L u 330 | GTG Val | CCC Pro | CAG Gln | CCT Pro | TTG Leu 335 | ` | 1128 |
| G V | TT | GAC Asp | TC Se | C T | Ar 1 | CGA Arg 340 | CAG Gln | CAG (Gln (| CAG Gln | CAG Gln | CAG Gln 345 | CAG (Gln) | CTC | CTA Leu | CAG Gln | AGG Arg 350 | CCG Pro | | 1176 |
| A | GT | CAC | CT | G C | AG (| CT | CCA, | TCC 1 | TAT | GGG | ccc (| GTG (| CTC ' | rcc | CCA | ATG | AAC | | 1224 |

| | Ser | His | Leu | 1 Glr 355 | Pro | Pro | Ser | Tyr | Gly 360 | Pro | Val | . Leu | ı Ser | Pro 365 | | Asn | | | |
|---|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-----|--------------|--|
| | AAG Lys | GTA Val | CAC His | s Gly | GGT Gly | GTC Val | AAC L Asn | AAA Lys 375 | Leu | CCC Pro | TCC Ser | GTC Val | AAC Asn 380 | Gln | CTG Leu | GTG Val | | 1272 | |
| | GGC Gly | G1: 385 | /Src | CCC Pro | CCG Pro | CAC His | AGC Ser 390 | Ser | GCA Ala | GCT Ala | Gly | Pro 395 | Asn | CTG Leu | GGG Gly | Pro | | 1320 | |
| | Met 400 | Gly | ' Ser | Gly | Met | 405 | | Ser | His | Gly | His 410 | Ser | Met | Pro | Ala | Asn 415 | | 1368 | |
| | GIĀ | Glu | Met | Asn | 450 G1A | Gly | CAC His | Ser | Ser | Gln 425 | Thr | Met | Val | Ser | Gly 430 | Ser | | 1416 | |
| | CAC | TGC Cys | ACC Thr | CCG Pro 435 | CCX Pro | Pro | Pro | TAT Tyr | CAT His 440 | GCA Ala | GAC Asp | CCC | AGC Ser | CTC Leu 445 | GTC Val | AGT Ser | | 1464 | |
| | Phe | Leu | Thr 450 | Gly | Leu | Gly | Cys | Pro 455 | Asn | Cys | Ile | Glu | Cys 460 | Phe | Thr | Ser | | 1512 | |
| | GIN | G1y 465 | Leu | Gln | Ser | Ile | TAC Tyr 470 | Nis | Leu | Gln | Asn | Leu 475 | Thr | Ile | Glu | Asp | | 1560 | |
| | 180 | GIĀ | Ala | Leu | Lys | Val 485 | Pro | Asp | GZn | Tyr | Arg 490 | Met | Thr | Ile | Trp | Arg 495 | | 1609 | |
| | / | Leu | Gin. | Asp | Leu 500 | Lys | CAG Gln | Ser | His | A 5 2 | Cys | Gly | Gln | Gln | Leu 510 | Leu | | 1656 | |
| ` | Arg | ser | ser | 515 | Asn | Ala | GCC Ala | Thr | 11e 520 | Ser | Ile | Gly | Gly | Ser 5,25 | Gly | Glu | | 1704 | |
| - | CTG Leu | CAG Gln | CGG Arg 530 | CAG Gln | CGG Arg | GTC Val | ATG Met | GAA Glu 535 | GCC Ala | GTG Val | CAT His | TTC Phe | CGT Arg 540 | GTG Val | CGC Arg | CAC His | | 1752 | |
| | inr | ATC Ile 545 | ACA Thr | ATC Ile | CCC Pro | AAC Asn | CGT Arg 550 | GGA Gly | G1 y GGC | GCA Ala | Gly | GCG Ala 555 | GTG Val | ACA Thr | GGT Gly | CCC Pro | | 1900 | |
| | GAC Asp 560 | GAG Glu | TGG Trp | GCG Ala | GAC Asp | TTT Phe 565 | GGC Gly | TTT Phe | GAC Asp | CTG Leu | CCT Pro 570 | GAC Asp | TGC Cys | AAG Lys | icc ser | CGT Arg 575 | | 1848 | |
| | AAG (Lys (| CAG Gln | CCC Pro | Ile | AAA Lys 580 | GAG Glu | GAG Glu | TTC . Phe | Thr | GAG Glu 585 | ACA Thr | GAG Glu | AGC Ser | CAC His | | | | 1890 | |
| | TGAG | GAAC | GT A | CCTT | CTTC | T CC | TGTC | CTTC | CTC | IGTG. | AGA | AACT | GCTC | TT G | GAAG | TGGGA | | 1950 | |
| | CCTG | TTGG | CT G | TGCC | CACA | g aa | ACCA | GCAA | GGA | CCTT | CTG | CCGG | ATGC | CA T | TCCT | gaagg | . \ | 2 010 | |
| • | GAAG? | rcgc' | TC A | TGAA | CTAA | c TC | CCTC | TTGG | | • | | | | | | | | 2040 | |
| | | | | | | | | • | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 8:

⁽i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 589 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala 20 25 30 Ser Pro TX Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr 65 70 75 80 Phe Gln Gln Ser Set Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln 100 105 Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro 145 150 155 160 Ala Ser His Leu Ile Arg Val Glu Glv Asn Asn Leu Ala Gln Tyr Val 165 170 175 Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Deu Tyr Asn Phe Met Cys 195 205 Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Aro Ile Leu Val Ile 210 220 Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe 225 235 240 Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu 245 250 255 Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn 260 265 270 Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro 275 Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met 290 295 300 Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys 305 310 315 320 Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys

Ser Pro Tyr thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro
45 Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn The Asp Tyr Pro Gly Pro His His Phe Glu Val Thr
65 75 80 Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln
100 105 110 Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys 130 140 Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro 145 155 160 Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val 165 170 175 Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro 180 185 190 Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys 195 200 Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Tle Leu Val Ile 210 220 Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu 255 Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn 260 265 270 Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro 275 280 285 Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met 290 295 300 Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val

Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu S r Pro Met Asn Lys

(ii) MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Cys\Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn

Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala

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Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro Met Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn Gly Gly Ser 405 Glu Met Asn\Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Gly Leu Gln Ser Ile Txr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu Arg Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu 515 Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg Lys Pro Ile Lys Glu Glu Phe Thr Glu Thr Glu Ger His

(2) INFORMATION FOR SEQ ID NO: 9:

580

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 758 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mus musculus
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 389..757
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGTCCCGCT TCGACCAAGA CTCCGGCTAC CAGCTTGCGG GCCCCGCGGA GGAGGAGACC CCGCTGGGGC TAGCTGGGCG ACGCGCGCCA AGCGGCGGCG GGAAGGAGGC GGGAGGAGCG GGGCCCGAGA CCCCGACTCG GGCAGAGCCA GCTGGGGAGG CGGGGCGCGC GTGGGAGCCA GGGGCCCGGG TGGCCGCCC TCCTCCGCCA CGGCTGAGTG CCCGCGCTGC CTTCCCGCCG

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| GTC | CGCC | AAG | AAAG | GCGC | TA A | GCCT | GCGG | C AG | TCCC | CTCG | cce | CCGC | CTC | CCTG | CTCC | €C 300 |
|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|--------------------|-------------------|---------------|
| ACC | CTTA | TAA | CCCG | CCGT | cc c | GCAT | CCAG | G CC | AGGA | GGCA | ACG | CTGC | AGC | CCAG | CCCTC | :G 360 |
| cce | ACGC | CGA | CGCC | CGGC | CC G | GAGC | AĢA | ATG Met 1 | AGC Ser | GGC Gly | AGC Ser | GTT Val 5 | GGG Gly | GAG Glu | ATG Met | 412 |
| GCC Ala | CAG Gln 10 | \Thr | TCT Ser | TCT Ser | TCC | TCC Ser 15 | TCC Ser | TCC Ser | ACC Thr | TTC Phe | GAG Glu 20 | His | CTG Leu | TGG Trp | AGT Ser | . 460 |
| TCT Ser 25 | Leu | GAG Glu | CCA Pro | GAC Asp | AGC Ser 30 | Thr | TAC Tyr | TTT Phe | GAC Asp | CTC Leu 35 | CCC Pro | CAG Gln | CCC Pro | AGC Ser | CAA Gln 40 | 508 |
| GGG Gly | ACT | AGC Ser | GAG Glu | GCA Ala 45 | TCA Ser | GGC Gly | AGC Ser | GAG Glu | GAG Glu 50 | TCC Ser | AAC Asn | ATG Met | GAT Asp | GTC Val 55 | TTC Phe | 556 |
| CAC His | CTG Leu | CAA Gln | GGC Gly 60 | ATG Met | GCC Ala | CAG Gln | TTC | AAT Asn 65 | TTG Leu | CTC Leu | AGC Ser | AGT Ser | GCC Ala 70 | ATG Met | GAC Asp | 604 |
| CAG Gln | ATG Met | GGC Gly 75 | AGC Ser | CGT Arg | GCG Ala | ACC Ala | CCG Pro 80 | GCG Ala | AGC Ser | CCC | TAC Tyr | ACC Thr 85 | CCG Pro | G AG Glu | CAC His | 652 |
| GCC Ala | GCC Ala 90 | AGC Ser | GCG Ala | CCC Pro | ACC Thr | CAC His 95 | icc ser | CCC Pro | TAC Tyr | GCG Ala | CAG Gln 100 | CCC | AGC Ser | TCC Ser | ACC Thr | 700 |
| TTC Phe 105 | GAC Asp | ACC Thr | ATG Met | TCT Ser | CCG Pro 110 | GCG Ala | CCT Pro | val orc | ATC Ile | CCT Pro 115 | TCC Ser | ÄAT Asn | ACC Thr | GAC Asp | TAC Tyr 120 | 748 |
| | GGC Gly | CCC Pro | C | 4 | | | | | | | | | | • | | 7.58 |

INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Gly Ser Val Gly Glu Met Ala Gln Thr Ser Ser Ser Ser 1 5 10

Ser Thr Phe Glu His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr 20 25 30

Phe Asp Leu Pro Gln Pro Ser Gln Gly Thr Ser Glu Ala Ser Gly Sex 35

Glu Glu Ser Asn Met Asp Val Phe His Leu Gln Gly Met Ala Gln Phe 50 55 60

Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro 65 70 75 80

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser 85 90 95

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro 105

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro 115 120 (2) INFORMATION FOR SEQ ID NO: 11: 1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 559 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (vi) ORIGNAL SOURCE: QRGANISM: Homo sapiens (A) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: CGACCTTCCC CAGTCAAGCC GGGGGAATAA TGAGGTGGTG GGCGGAACGG ATTCCAGCAT 60 GGACGTCTTC CACCTGGAGG GCATGACTAC ATCTGTCATG CATCCTCGGC TCCTGCCTCA 120 CTAGCTGCGG AGCCTCTCCC CCTCGGTCCA CGCTGCCGGG CGGCCACGAC CGTGACCCTT 180 CCCCTCGGGC CGCCCAGATC CATGCCTCGT CCCACGGGAC ACCAGTTCCC TGGCGTGTGC 240 AGACCCCCCG GCGCCTACCA TGCTGTACGT CGGTGACCCC GCACGGCACC TCGCCACGGC 300 CCAGTTCAAT CTGCTGAGCA GCACCATGGA CCAGATGAGC AGCCGCGGG CCTCGGCCAG 360 CCCCTACACC CCAGAGCACG CCGCCAGCGT GCCCACCCAC TCGCCCTACG CACAACCCAG 420 CTCCACCTTC GACACCATGT CGCCGGCGCC TGTCATCCCC TCCAACACCG ACTACCCCGG 480 ACCCCACCAC TITGAGGICA CTTTCCAGCA GTCAGCACG GCCAAGTCAG CCACCTGGAC 540 GTACTCCCCG CTCTTGAAG 559 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: (A) LENGTH: 1764 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: ATGCTGTACG TCGGTGACCC CGCACGGCAC CTCGCCACGG CCCAGTTCAA TCTGTGAGC 60 AGCACCATGG ACCAGATGAG CAGCCGCGCG GCCTCGGCCA GCCCCTACAC CCCAGAGCAC 120 GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG 180 TCGCCGGCGC CTGTCATCCC CTCCAACACC GACTACCCCG GACCCCACCA CTTTGAGGTC 240

ACTITCCAGO AGTOCAGOAC GGCCAAGTOA GCCACOTGGA CGTACTCCCC GCTOTTGAAG

AAACTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCCGCCA

CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC

GTCGTGAAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTGCT

300

3/60

420

CCAGCCAGCC ACCTCATCCG CGTGGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT 540 GTCACCGGCA GGCAGAGCGT CGTGGTGCCC TATGAGCCAC CACAGGTGGG GACGGAATTC 600 ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGGCGG 660 CCCATCCTOA TCATCATCAC CCTGGAGATG CGGGATGGGC AGGTGCTGGG CCGCCGGTCC 720 GCATCTGCGC CTGTCCTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC TTTGAGGGCC 780 CGGGAGCAGC AGGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 940 TTCAAGCAGA GCCCQCCTGC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGGCGGCAT 900 GGAGACGAGG ACACGTÀCTA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 96Ò AAGCTGAAAG AGAGCCTGÒA GCTGATGGAG TTGGTGCCGC AGCCACTGGT GGACTCCTAT 1020 CGGCAGCAGC AGCAGCTCCT ACAGAGGCCG AGTCACCTAC AGCCCCCGTC CTACGGGCCG 1080 GTCCTCTCGC CCATGAACAA GOTGCACGGG GGCATGAACA AGCTGCCCTC CGTCAACCAG 1140 CTGGTGGGCC AGCCTCCCCC GCACAGTTCG GCAGCTACAC CCAACCTGGG GCCCGTGGGC 1200 CCCGGGATGC TCAACAACCA TGGCCAGGCA GTGCCAGCCA ACGGCGAGAT GAGCAGCAGC 1260 CACAGCGCCC AGTCCATGGT CTCGGGGTTGC CACTGCACTC CGCCACCCCC CTACCACGCC 1320 GACCCCAGCC TCGTCAGTTT TTTAACAGGA TTGGGGTGTC CAAACTGCAT CGAGTATTTC 1380 ACCTCCCAAG GGTTACAGAG CATTTACCAC CTGCAGAACC TGACCATTGA GGACCTGGGG 1440 GCCCTGAAGA TCCCCGAGCA GTACCGCATG ACCARCTGGC GGGGCCTGCA GGACCTGAAG 1500 CAGGGCCACG ACTACAGCAC CGCGCAGCAG CTGCTCCGCT CTAGCAACGC GGCCACCATC 1560 TCCATCGGCG GCTCAGGGGA ACTGCAGCGC CAGCGGGTC% TGGAGGCCGT GCACTTCCGC 1620 GTGCGCCACA CCATCACCAT CCCCAACCGC GGCGGCCCAG GCGGCGGCCC TGACGAGTGG 1680 GCGGACTTCG GCTTCGACCT GCCCGACTGC AAGGCCCGCA AGQAGCCCAT CAAGGAGGAG 1740 TTCACGGAGG CCGAGATCCA CTGA 1764

INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:.

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Ahe

Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser

Pro Tyr Ala Gin Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val

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Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile th lie Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Agn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr 165 170 Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met 195 200 Cys Asn Ser Ser Cys val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile 210 220 Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser 225 230 235 240 Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp
245 250 255 Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala the Lys Gln Ser Pro Pro Ala Val 275 280 285 Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp 290 295 Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met 305 310 320 Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Let Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gan Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Wal Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly 385 Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His Qys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu 440 Thr Gly Leu Gly Cys Pro Asn Cys Il Glu Tyr Phe Thr Ser Gln Gly

| Leu 465 | Gl'n | Ser | Ile | Tyr | His 470 | Leu | Gln | Asn | Leu | Thr 475 | Ile | Glu | Asp | | Gly 480 |
|------------|------------|------------|-------------|------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|
| | • | | | Pro 485 | | | | | 490 | | | | | 495 | |
| 3½n | Ąsp | Leu | Lys 500 | Gln | GÌγ | His | Ąśp | Tyr 505 | Ser | Thr | Ala | Gln | Gln 510 | Leu | Leu |
| Arg | ser | Ser 515 | Asn | Ala | Ala | Thr | Ile 520 | Ser | Ile | Gly | Ġly | Ser 525 | Gly | Glu | Leu |
| Gln | Arg 530 | eyb. | Arg | Val | Met | Glu 535 | Ala | Val | His | Phe | Arg 540 | Val | Arg | His | Thr |
| Ile 545 | Thr | Ile | P 20 | Asn | Arg 550 | Gly | Gly | Pro | Gly | Gly 555 | Gly | Pro | Asp | Glu | Trp 560 |
| Ala | Asp | Phe | Gly | Phe 565 | qeA | Leu | Pro | Asp | Су з 570 | Lys | Ala | Arg | Lys | Gln 575 | Pro |
| Ile | Lys | Glu | Glu 580 | Phe | Mr | Glu | Ala | Glu 585 | Ile | His | | | | | |

(2) INFORMATION FOR SEQ ID NO. 14:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1521 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 14

| I | | | | - , | / | | |
|---|------------|------------|------------|------------|------------|-------------------|-------|
| Ø | ATGCTGTACG | TCGGTGACCC | CGCACGGCAC | CTCGCCACGG | CCCAGTTCAA | . TCTGCTGAGC | 60 |
| | AGCACCATGG | ACCAGATGAG | CAGCCGCGCG | GCCTCGGCCA | GCCCCTACAC | CCCAGAGCAC | 120 |
| | GCCGCCAGCG | TGCCCÁCCCA | CTCGCCCTAC | GCACAACCCA | GCTCCACCTT | CGACACCATG | 130 |
| | TCGCCGGCGC | CTGTCATCCC | CTCCAACACC | GACTACCCCG | GACCCCACCA | CTTTGAGGTC | 240 |
| | ACTTTCCAGC | AGTCCAGCAC | GGCCAAGTCA | GCCACCTGGA | CGTACTCCCC | OCTOTIGAAG | 300 |
| | AAACTCTACT | GCCAGATCGC | CAAGACATGC | CCCATCCAGA | TCAAGGTGTC | CACCCGCCA | 360 |
| | CCCCCAGGCA | CTGCCATCCG | GGCCATGCCT | GTTTACAAGA | AAGCGGAGCA | CGTGACGAC | 42Ô |
| | GTCGTGAAAC | GCTGCCCCAA | CCACGAGCTC | GGGAGGGACT | TCAACGAAGG | ACAGTCTOCT | 480 |
| | CCAGCCAGCC | ACCTCATCCG | CGTGGAAGGC | AATAATCTCT | CGCAGTATGT | GGATGACCCT | 540 |
| | GTCACCGGCA | GGCAGAGCGT | CGTGGTGCCC | TATGAGCCAC | CACAGGTGGG | GACGGAATTC | 600 |
| | ACCACCATCC | TGTACAACTT | CATGTGTAAC | AGCAGCTGTG | TAGGGGGCAT | GAACCGGCGG | 660 |
| | CCCATCCTCA | TCATCATCAC | CCTGGAGATG | CGGGATGGGC | AGGTGCTGGG | CCGCCGGTCC | 720 |
| • | TTTGAGGGCC | GCATCTGCGC | CTGTCCTGGC | CGCGACCGAA | AAGCTGATGA | GGACCACTAC | . 780 |
| (| CGGGAGCAGC | AGGCCCTGAA | CGAGAGCTCC | GCCAAGAACG | GGGCCGCCAG | CAAGCGTGCC | 940 |
| • | TTCAAGCAGA | GCCCCCTGC | CGTCCCCGCC | сттестессе | GTGTGAAGAA | GCGGCGGCAT | 900 |
| (| GGAGACGAGG | ACACGTACTA | CCTTCAGGTG | CGAGGCCGGG | AGAACTTTGA | GATCCTGATG | 960 |

| AAGCTGAAAG | AGAGCCTGGA | GCTGATGGAG | TTGGTGCCGC | AGCCACTGGT | GGACTCCTAT | 102 |
|------------------------------|------------|------------|------------|------------|------------|------|
| CGGCAGCAGC | AGCAGCTCCT | ACAGAGGCCG | CCCCGGGATG | CTCAACAACC | ATGGCCACGC | 108 |
| дот о сса сс с | AACGGCGAGA | TGAGCAGCAG | CCACAGCGCC | CAGTCCATGG | TCTCGGGGTC | 1140 |
| ссастэсаст | CCGCCACCCC | CCTACCACGC | CGACCCCAGC | CTCGTCAGGA | CCTGGGGGCC | 1200 |
| CTGAAGATÇC | CCGAGCAGTA | CCGCATGACC | ATCTGGCGGG | GCCTGCAGGA | CCTGAAGCAG | 1260 |
| GGCCACGACT | ACAGCACCGC | GCAGCAGCTG | CTCCGCTCTA | GCAACGCGGC | CACCATCTCC | 1320 |
| ATCGGCGGCT | CAGGGGAACT | GCAGCGCCAG | CGGGTCATGG | AGGCCGTGCA | CTTCCGCGTG | 1380 |
| CGCCACACCA | TCACCATCCC | CAACCGCGGC | GGCCCAGGCG | GCGGCCCTGA | CGAGTGGGCG | 1440 |
| GACTTCGGCT | TCGACQTGCC | CGACTGCAAG | GCCCGCAAGC | AGCCCATCAA | GGAGGAGTTC | 1500 |
| ACGGAGGCCG | AGATCCACTG | A | | | | 1521 |

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Phe

Asn Leu Leu Ser Ser Thr Met Asp Gin Met Ser Ser Arg Ala Ala Ser

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro 50 55

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro Xis His Phe Glu Val 65

Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser

Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thi Cys Pro Ile 100

Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala

Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg 135

Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala 150

Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr

Val Asp Asp Pro Val Thr Gly Arg Gln S r Val Val Pro Tyr Glu

Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met

Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asa His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Aly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser\Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gla Gln Gln Leu Leu Gln Arg Pro Pro Arg 340 Asp Ala Gln Gln Pro Trp Pko Arg Ser Ala Ser Gln Arg Arg Asp Glu Gln Gln Pro Gln Arg Pro Val Ais Gly Leu Gly Val Pro Leu His Ser Ala Thr Pro Leu Pro Arg Arg Pro Gln Pro Arg Gln Asp Leu Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln 405 Asp Leu Lys Gln Gly His Asp Tyr Ser The Ala Gln Gln Leu Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile

(2) INFORMATION FOR SEQ ID NO: 16:

500

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1870 base pairs

Lys Glu Glu Phe Thr Glu Ala Glu Ile His

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

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|---|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|-------------|
| | TGO | ccg | GGC | TGC | AÇGO | cir c | CAGO | GAAC | C AG | ACAG | CACC | TAC | TTCG | ACC | TTCC | CCAG | TC | 60 |
| | AAG | ccsc | :gec | AATA | ATG# | IGG 1 | GGTC | GGCG | G AA | ADDO. | TTCC | AGC | | | | TTC Phe | | 115 |
| | CAC His | Let | GAC Glu | i of h | ATC Met | ACT Thr 10 | Thr | TCT Ser | GTC Val | ATG Met | GCC Ala 15 | Gln | TTC Phe | AAT Asn | CTG Leu | CTG Leu 20 | | 163 |
| | Ser | Ser | Thi | ATG Met | A\9 p 2\5 | Gln \ | Met | Ser | Ser | Arg 30 | Ala | Ala | Ser | Ala | Ser 35 | Pro | | 211 |
| | Tyr | Thr | Pro | GAG Glu 40 | His | Alla | Ala \ | Ser | Val 45 | Pro | Thr | His | Ser | Pro 50 | Tyr | Ala | | 259 |
| | Gln | Pro | Ser 55 | | Thr | Phe | Asp | Thr 60 | Met | Ser | Pro | Ala | Pro 65 | Val | Ile | Pro | | 307 |
| | Ser | Asn 70 | Thr | GAC Asp | Tyr | Pro | Gly 75 | Pho | His | His | Phe | Glu 80 | Val | Thr | Phe | Gln | | 355 |
| | Gln 85 | Ser | Ser | ACG Thr | Ala | 90 | Ser | Ala | THE | Trp \ | Thr 95 | Tyr | Ser | Pro | Leu | Leu 100 | | 403 |
| | Lys | Lys | Leu | TAC Tyr | Cys 105 | Gln | Ile | Ala | Lys | Th 110 | Суз | Pro | Ile | Gln | Ile 115 | Lys | . 5 | 451 |
| | GTG Val | TCC Ser | ACC Thr | CCG Pro 120 | CCA Pro | CCC Pro | CCA Pro | GGC Gly | ACT Thr 125 | GCC Ala | ATC 11d | CGG Arg | GCC Ala | ATG Met 130 | CCT | GTT Val | | 499 |
| (| TAC Tyr | AAG Lys | AAA Lys 135 | GCG Ala | GAG Glu | CAC His | GTG Val | ACC Thr 140 | GAC Asp | GTC Val | GTG Val | AAA Lys | CGC Arg 145 | TGC Cys | CCC Pro | AAC Asn | | 547 |
| , | CAC His | GAG Glu 150 | CTC Leu | GGG Gly | AGG Arg | GAC Asp | TTC Phe 155 | AAC Asn | GAA Glu | GGA Gly | CAG Gln | TCT Ser 160 | GC/T Ala | CCA Pro | GCC Ala | AGC Ser | | 595 |
| | CAC His 165 | | ATC Ile | CGC Arg | GTG Val | GAA Glu 170 | GGC Gly | AAT Asn | AAT Asn | CTC Leu | TCG Ser 175 | CAG Gln | TAT Tyr | GTG Val | GAT Asp | GAC Asp 180 | | 643 |
| | CCT Pro | GTC Val | ACC Thr | GGC Gly | AGG Arg 185 | CAG Gln | AGC Ser | GTC Val | GTG Val | GTG Val 190 | CCC Pro | TAT Tyr | GAG Glu | CCA Pro | CCA Pro 195 | CAG Gln | | 691 |
| | GTG Val | GGG Gly | ACG Thr | GAA Glu 200 | TTC Phe | ACC | ACC Thr | ATC Ile | CTG Leu 205 | TAC Tyr | AAC Asn | TTC Phe | ATG Met | TGT Cys 210 | AAC Asn | AGC Sei | \ | 739 |
| | AGC Ser | TGT Cys | GTA Val 215 | GGG Gly | GGC Gly | ATG Met | AAC Asn | CGG Arg 220 | CGG Arg | CCC Pro | ATC Il | CTC | ATC Ile 225 | ATC Ile | ATC Ile | ACC Thr | | 78 7 |
| | CTG Leu | GAG Glu 230 | ATG Met | CGG Arg | GAT Asp | GGG GGG | CAG Gln 235 | GTG Val | CTG Leu | GGC Gly | CGC Arg | CGG Arg 240 | TCC Ser | TTT Phe | GAG Glu | GGC Gly | ` | 835 |
| | CGC | ATC | TGC | GCC | TGT | CCT | GGC | CGC | GAC | CGA | AAA | GCT | GAT | GAG | GAC | CAC | | 883 |

| | Ar 24 | g Il 5 | e C | /s A | la C | ys Pr 25 | 60 Gl | y Ar | g As | p Ar | g Lys 255 | s Al | a As | p Gl | u As | p His | |
|---|-------------------|-------------------|--------------------|--------------------|-------------------------|----------------------|-----------------------|-----------------------|-------------------|-----------------------|-------------------|-------------------|---------------------|-------------------|--------------------|---------------------|------|
| | TA Ty | c co | iG GI ig GI | AG C. Lu G | ın .G. | AG GC ln Al 65 | C CT .a Le | G AAG u Asr | GA(| G AG0 u Sei 270 | : Ser | GC Al | C AAG a Ly | G AA s As | C GG n G1 27 | G GCC y Ala 5 | 931 |
| | Αſ | a Se | r Ly | /S\A. | rg Al 30 \ | la Ph | e Ly: | s Glr | 1 Sea 285 | r Pro |) Pro | Ala | a Val | 1 Pro 290 | o Al | C CTT a Leu | |
| | GG G1 | T GC y Al | C GC a Gl 29 | y Va | IQ AA | AG AA /s Ly | G CGG | G CGG G Arg 300 | , His | GGA Gly | A GAC | GAC Glu | GA0 1 Asp 305 | Th | TAC | C TAC r Tyr | 1027 |
| | CT' Le | CA 1 Gl 31 | n Va | 'G C(| GA GC | y CG | G GAG g Glu 315 | ı Asn | TTT Phe | GAG Glu | ATC | Leu 320 | ı Met | AAC Lys | G CTO | G AAA u Lys | 1075 |
| | GA0 G1: 325 | 1 5e | C CT r Le | G GA u Gl | AG CI .u Le | G AT u Me 33 | t \ Gli | TTG Leu | GTG Val | CCG Pro | CAG Gln 335 | Pro | CTG Leu | GTC Val | GA(. Asi | TCC Ser 340 | 1123 |
| | TA1 | CGG Arc | G CA g Gl | G CA n Gl | G CA n Gl 34 | n Gl | G CTO | CTA | CAG Gln | AGG Arg 350 | Pro | AGT Ser | CAC His | CTA Leu | CAC Glr 355 | G CCC n Pro | 1171 |
| | Pro | Sei | TA Ty | C GG r G1 36 | y Pr | G GT(o Vai | C CTC L Leu | TCO Ser | CCC Pro 365 | Met | AAC Asn | AAG Lys | GTG Val | CAC His | Gly | GGC Gly | 1219 |
| | ATG Met | AAC Asr | AA0 1 Ly: 37 | s Le | G CC u Pr | C TCC | GTC Val | AAC Asn 380 | CAG Gln | CTG | GTG Val | GGC Gly | CAG Gln 385 | CCT | CCC | CCG Pro | 1267 |
| | CAC | AGT Ser 390 | : Se | c AI | A GC' a Al | T ACA | CCC Pro 395 | AAC Asn | CTG Leu | GGG Gly | ÇCC P¥0 | GTG Val 400 | Gly | CCC | GGG Gly | ATG Met | 1315 |
| | CTC Leu 405 | AAC Asn | AA0 Asr | CA' | T GG(s Gl; | CAC Y His 410 | GCA Ala | GTG Val | CCA Pro | GCC Ala | AAC Asn 415 | ej gec | GAG Glu | ATG Met | AGÇ Ser | AGC Ser 420 | 1363 |
| ` | AGC Ser | CAC | AGC Ser | GCC | CAC a Glr 425 | ı Ser | ATG Met | GTC Val | TCG Ser | GGG Gly 430 | TCC Ser | CAC His | Tec cys | ACT Thr | CCG Pro 435 | | 1411 |
| | CCC Pro | CCC Pro | TAC | Hi: | S ALA | GAC Asp | Pro | AGC Ser | CTC Leu 445 | GTC Val | AGT Ser | TTT Phe | TTA Leu | ACA Thr 450 | Gly | TTG Leu | 1459 |
| | GGG Gly | TGT Cys | Pro 455 | M3I | TGC Cys | ATC Ile | GAG Glu | TAT Tyr 460 | TTC Phe | ACC Thr | TCC Ser | CAA Gln | GGG Gly 465 | TTA Leu | CAG Gln | AGC | 1507 |
| | ATT Ile | TAC Tyr 470 | CAC His | CTC | CAG Gln | AAC Asn | CTG Leu 475 | ACC Thr | ATT Ile | GAG Glu | GAC Asp | CTG Leu 480 | GGG Gly | GCC Ala | CTG Leu | AAG Lys | 1555 |
| | ATC Ile 485 | CCC Pro | GAG Glu | CAG Gln | TAC Tyr | CGC Arg 490 | ATG Met | ACC Thr | ATC Ile | TGG Trp | CGG Arg 495 | GGC G1 y | CTG Leu | CAG Gln | GAC Asp | CTG Leu 500 | 1603 |
| 4 | AAG Lys | CAG Gln | GGC Gly | CAC | GAC Asp 505 | TAC Tyr | AGC Ser | ACC Thr | Ala | CAG Gln 510 | CAG Gln | CTG Leu | CTC Leu | CGC Arg | TCT Ser 515 | AGC Ser | 1651 |
| 1 | AAC Asn | GCG Ala | GCC Ala | ACC Thr 520 | TIE | TCC Ser | ATC Ile | GIA | GGC Gly 525 | TCA Ser | GGG (Gly (| GAA Glu | Leu | CAG Gln 530 | CGC Arg | CAG Gln | 1699 |
| (| CGG | GTC | ATG | GAG | GCC | GTG | CAC | TTC | CGC | GTG (| CGC (| CAC | ACC | ATC | ACC | ATC | 1747 |

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E.

Arg Val Met 535 Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile

CCC AAC CGC GGC GGC CCA GGC GGC GGC CCT GAC GAG TGG GCG GAC TTC
Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala Asp Phe
550

GGC TTC GAC CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG
Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu
565

GAG TTC ACG GAG GCC GAG ATC CAC TGA
Glu Phe Thr Glu Ala Glu Ile His
585

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
1 10 15

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala 20 30

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His

Ser Pro Tyr Ala Gln Pro Ser Ser Thr the Asp Thr Met Ser Pro Ala
50 55

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 65 70 80

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
85 90 95

Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg 115

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
130 135 140

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser 150 155 160

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln 165

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Pro Tyr

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Led 210 220

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg 235 240

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Cou Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu 290 295 300 Asp Thr Tyr Tyx Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys 355 360 365 Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn His\Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser Ser His Ser Ala Gn Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln 450 Aly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu 465 470 480 Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu 500 505 Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1817 base pairs

Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MQLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

| | • | \ | | - - | • | • | |
|---|--------------|------------|------------|------------|------------|--------------|-------|
| | ATGGCCCAGT | CCACCGCKAC | CTCCCCTGAT | GGGGGCACCA | CGTTTGAGC | A CCTCTGGAGC | 60 |
| | TCTCTGGAAC | CAGACAGCA | CTACTTCGAC | CTTCCCCAGT | CAAGCCGGG | GAATAATGAG | 120 |
| | GTGGTGGGCG | GAACGGATTC | CAGCATGGAC | GTCTTCCACC | TGGAGGGCA | GACTACATCT | 180 |
| | GTCATGGCCC | AGTTCAATCT | GTGAGCAGC | ACCATGGACC | AGATGAGCAG | ccccccccc | 240 |
| | TCGGCCAGCC | CCTACACCC | AGAGCACGCC | GCCAGCGTGC | CCACCCACTO | GCCCTACGCA | 300 |
| | CAACCCAGCT | CCACCTTCGA | CACCATGTCG | CCGGCGCCTG | TCATCCCCT | CAACACCGAC | 360 · |
| | TACCCCGGAC | CCCACCACTT | TGAGGTÇACT | TTCCAGCAGT | CCAGCACGG | CAAGTCAGCC | 420 |
| | ACCIGGACGT | ACTCCCCGCT | CTTGAAGAAA | CTCTACTGCC | AGATCGCCAA | GACATGCCCC | 480 |
| | ATCCAGATCA | AGGTGTCCAC | CCCGCCACCO | CCAGGCACTG | CCATCCGGG | CATGCCTGTT | 540 |
| | TACAAGAAAG | CGGAGCACGT | GACCGACGTC | GTGAAACGCT | GCCCCAACCA | CGAGCTCGGG | 600 |
| | ĄGGGACTTCA | ACGAAGGACA | GTCTGCTCCA | GCRAGCCACC | TCATCCGCGT | GGAAGGCAAT | 660 |
| | AATCTCTCGC | AGTATGTGGA | TGACCCTGTC | ACCOGCAGGC | AGAGCGTCGT | GGTGCCCTAT | 720 |
| | GAGCCACCAC | AGGTGGGGAC | GGAATTCACC | ACCATOCTGT | ACAACTTCAT | GTGTAACAGC | 780 |
| | AGCTGTGTAG | GGGGCATGAA | ccecceccc | ATCCTCATCA | TCATCACCCT | GGAGATGCGG | 840 |
| | GATGGGCAGG | TGCTGGGCCG | CCGGTCCTTT | GAGGGCCGCA | TCTGCGCCTG | TCCTGGCCGC | 900 |
| | GACCGAAAAG | CTGATGAGGA | CCACTACCGG | GAGCAGCAGG | CCCTGAACGA | GAGCTCCGCC | 960 |
| / | AAGAACGGGG | CCGCCAGCAA | GCGTGCCTTC | AAGCAGAGCC | cdccreccer | CCCCGCCCTT | 1020 |
| | GGTGCCGGTG | TGAAGAAGCG | GCGGCATGGA | GACGAGGACA | CGTACTACCT | TCAGGTGCGA | 1080 |
| | GGCCGGGAGA | ACTTTGAGAT | CCTGATGAAG | CTGAAAGAGA | GCCTGGAGCT | GATGGAGTTG | 1140 |
| | GTGCCGCAGC | CACTGGTGGA | CTCCTATCGG | CAGCAGCAGC | AGCTCCTACA | GAGGCCGAGT | 1200 |
| | CACCTACAGC | CCCCGTCCTA | CGGGCCGGTC | CTCTCGCCCA | TGAACAAGOT | GCACGGGGGC | 1260 |
| | ATGAACAAGC | TGCCCTCCGT | CAACCAGCTG | GTGGGCCAGC | CTCCCCGCA | CAGTTCGGCA | 1320 |
| | GCTACACCCA | ACCTGGGGCC | CGTGGGCCCC | GGGATGCTCA | ACAACCATGG | COACGCAGTG | 1,380 |
| | CCAGCCAACG | GCGAGÁTGAG | CAGCAGCCAC | AGCGCCCAGT | CCATGGTCTC | GGGTCCCAC | 1440 |
| | TGCACTCCGC | CACCCCCTA | CCACGCCGAC | CCCAGCCTCG | TCAGGACCTG | GGGGCCTGA | 1500 |
| | AGATCCCCGA (| GCAGTACCGC | ATGACCATCT | GGCGGGGCCT | GCAGGACCTG | AAGCAGGGCC | 1560 |
| | ACGACTACAG (| CACCGEGCAG | CAGCTGCTCC | GCTCTAGCAA | CGCGGCCACC | ATCTCCATC | 1620 |
| | GCGGCTCAGG (| GGAACTGCAG | CGCCAGCGGG | TCATGGAGGC | CGTGCACTTC | CGCGTGCGCC | 1680 |
| | ACACCATCAC (| CATCCCCAAC | CGCGGCGGCC | CAGGCGGCGG | CCCTGACGAG | TGGGCGGACT | 1740 |
| | TCGGCTTCGA (| CTGCCCGAC | TGCAAGGCCC | GCAAGCAGCC | CATCAAGGAG | GAGTTCACGG | 1800 |
| | AGGCCGAGAT C | CACTGA | • | | | | 18 7 |
| | | | | | | | ` |

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (11) MQLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Ala Gla Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro

Gln Ser Ser Arg\Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser

Met Asp Val Phe Hits Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln

Phe Asn Leu Leu Ser ger Thr Met Asp Gln Met Ser Ser Arg Ala Ala

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr

Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Led Tyr Asn Phe

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Ly& Ala

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala

Lys kan Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lxs Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly 450 Glu Met Ser Ser Ser His Ser Ala\Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr 485 490 Trp Gly Pro

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

GCGAGCTGCC CTCGGAG

- (2) INFORMATION FOR SEQ ID NO: 21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGTTCTGGAG GTGACTCAG (2) INFORMATION FOR SEQ ID NO: 22: (i) SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs. TYPE: nucleic acid (B) STRANDEDNESS: single (D) TOROLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: NO (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 22: GCCATGCCTG TCTACAAG (2) INFORMATION FOR SEQ ID NO: 23: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO 23: ACCAGCTGGT TGACGGAG (2) INFORMATION FOR SEQ ID NO: 24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24: GTCAACCAGC TGGTGGGCCA G (2) INFORMATION FOR SEQ ID NO: 25: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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TOPOLOGY: linear
                (ii) MOLECULE TYPE: DNA
               (iii) ANTI-SANSE: NO
                (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
            AGGCCGGCGT GGGGAAG
            (2) INFORMATION FOR SEQ ID NO: 27:
(i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 19 pase pairs
f. ±
                      (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
I, M
                      (D) TOPOLOGY: linear
                (ii) MOLECULE TYPE: DNA
               (iii) ANTI-SENSE: YES
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
           CTTGGCGATC TGGCAGTAG
           (2) INFORMATION FOR SEQ ID NO: 28:
                 (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 17 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: single
                      (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: DNA
              (iii) ANTI-SENSE: NO
               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
          GCGGCCACGA CCGTGAC
           (2) INFORMATION FOR SEQ ID NO: 29:
                (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 18 base pairs
                     (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: single
                     (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: DNA
              (iii) ANTI-SENSE: YES
```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GTGGATCTCG GCCTCC

(2) INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

16

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GGCAGCTTGG GTCTCTGG
                                                                            18
 (2) INFORMATION FOR SEQ ID NO: 30:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LINGTH: 18 base pairs (B) TYRE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (11) MOLECULE TYPE: DNA
    (iii) ANTI-SENSE: NO
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
CTGTACGTCG GTGACCCC
(2) INFORMATION FOR SEQ ID NO: 31:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 18 base paixs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
   (iii) ANTI-SENSE: YES
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
TCAGTGGATC TCGGCCTC
                                                                           18
    INFORMATION FOR SEQ ID NO: 32:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 18 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
   (iii) ANTI-SENSE: NO
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
AGGGGACGCA GCGAAACC
                                                                           18
(2) INFORMATION FOR SEQ ID NO: 33:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 19 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
   (iii) ANTI-SENSE: YES
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

19

CCATÇAGCTC CAGGCTCTC (2) INTORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (A) TOPOLOGY: linear (11) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: CCAGGACAGG CGCAGATG 18 (2) INFORMATION FOR SEQ ID NO: 35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: \ingle (D) TOPOLOGY: lineal (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35: GATGAGGTGG CTGGCTGGA 19 (2) INFORMATION FOR SEQ ID NO: 36: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36: TGGTCAGGTT CTGCAGGTG 19 (2) INFORMATION FOR SEQ ID NO: 37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (i1) MOLECULE TYPE: DNA (111) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

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CACCTACTC AGGGATGC
                                                                                  18 .
 (2) INFORMATION FOR SEQ ID NO: 38:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 21 base pairs
            (B) TYPE: nucleic acid (C) STRANDEDNESS: single
                TOPOLOGY: linear
            (D)
      (ii) MOLECULE TYPE: DNA
    (iii) ANTI-SENSE: YES
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 AGGAAAATAG AAGCGTCAGT C
                                                                                . 21
 (2) INFORMATION FOR SEQ ID NO: 39:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DN
    (iii) ANTI-SENSE: NO
     (xi) SEQUENCE DESCRIPTION:\seq ID NO: 39:
CAGGCCCACT TGCCTGCC
                                                                                  18
(2) INFORMATION FOR SEQ ID NO: 40:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19 base pair
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
    (iii) ANTI-SENSE: YES
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
CTGTCCCCAA GCTGATGAG
                                                                                  19
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